

(sample of submitted file)

Structure Explorer - 1RYP

Title Crystal Structure Of The 20S Proteasome From Yeast At 2.4 Angstroms Resolution
Classification Multicatalytic Proteinase
Compound Mol Id: 1; Molecule: 20S Proteasome; Chain: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U, V, W, X, Y, Z, 1, 2; Ec: 3.4.99.46; Mutation: Chains H, V, T1A, Chain L, Z, K33R; Biological Unit: Yeast Proteasome Seems To Be Composed Of 14 Different Subunits Which Form A Highly Ordered Ring-Shaped Structure
Exp. Method X-ray Diffraction

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Summary InformationView StructureDownload/Display FileStructural NeighborsGeometryOther SourcesSequence Details

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HEADER      MULTICATALYTIC PROTEINASE                      26-FEB-97    1RY
TITLE       CRYSTAL STRUCTURE OF THE 20S PROTEASOME FROM YEAST AT 2
TITLE       2 ANGSTROMS RESOLUTION
COMPND      MOL_ID: 1;
COMPND      2 MOLECULE: 20S PROTEASOME;
COMPND      3 CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P,
COMPND      4 R, S, T, U, V, W, X, Y, Z, 1, 2;
COMPND      5 EC: 3.4.99.46;
COMPND      6 MUTATION: CHAINS H, V, T1A, CHAIN L, Z, K33R;
COMPND      7 BIOLOGICAL_UNIT: YEAST PROTEASOME SEEMS TO BE COMPOSED
COMPND      8 14 DIFFERENT SUBUNITS WHICH FORM A HIGHLY ORDERED
COMPND      9 RING-SHAPED STRUCTURE
SOURCE      MOL_ID: 1;
SOURCE      2 ORGANISM_SCIENTIFIC: SACCHAROMYCES CEREVISIAE;
SOURCE      3 ORGANISM_COMMON: BAKER'S YEAST
KEYWDS      MULTICATALYTIC PROTEINASE, 20S PROTEASOME, PROTEIN
KEYWDS      2 DEGRADATION, ANTIGEN PROCESSING, HYDROLASE, PROTEASE
EXPDTA      X-RAY DIFFRACTION
AUTHOR      M.GROLL,L.DITZEL,J.LOEWE,D.STOCK,M.BOCHTLER,H.D.BARTUNI
AUTHOR      2 R.HUBER
REVDAT      1 15-APR-98 1RYP 0
JRNL        AUTH M.GROLL,L.DITZEL,J.LOWE,D.STOCK,M.BOCHTLER,
JRNL        AUTH 2 H.D.BARTUNIK,R.HUBER
JRNL        TITL STRUCTURE OF 20S PROTEASOME FROM YEAST AT 2.4
JRNL        TITL 2 RESOLUTION
JRNL        REF NATURE V. 386 463 199
JRNL        REFN ASTM NATUAS UK ISSN 0028-0836
REMARK      1
REMARK      2
REMARK      2 RESOLUTION. 1.9 ANGSTROMS.
REMARK      3
REMARK      3 REFINEMENT.
REMARK      3 PROGRAM : X-PLOR 3.1
REMARK      3 AUTHORS : BRUNGER
REMARK      3
REMARK      3 DATA USED IN REFINEMENT.
REMARK      3 RESOLUTION RANGE HIGH (ANGSTROMS) : 1.9
REMARK      3 RESOLUTION RANGE LOW (ANGSTROMS) : 50.
REMARK      3 DATA CUTOFF (SIGMA(F)) : 2.
REMARK      3 DATA CUTOFF HIGH (ABS(F)) : 100000000.
REMARK      3 DATA CUTOFF LOW (ABS(F)) : 0.1
REMARK      3 COMPLETENESS (WORKING+TEST) (%) : 90.5
REMARK      3 NUMBER OF REFLECTIONS : 752101
REMARK      3
REMARK      3 FIT TO DATA USED IN REFINEMENT.
REMARK      3 CROSS-VALIDATION METHOD : NULL
```